CLAIM AMENDMENTS

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (withdrawn) An array composition comprising:

a) a substrate with a surface comprising discrete sites; and

b) a population of microspheres comprising at least a first and a second subpopulation, wherein the microspheres of each subpopulation each comprise a plurality of target analytes;

wherein said microspheres are distributed on said surface.

2. (withdrawn) The array composition according to claim 1 wherein said microspheres of each subpopulation further comprise an optical signature.

3. (withdrawn) The array composition according to claim 1 wherein said microspheres of each subpopulation further comprise an identifier binding ligand.

4. (withdrawn) The array composition according to claim 3 wherein said identifier binding ligand is a nucleic acid.

5. (withdrawn) The array composition according to claim 1 wherein said target analytes are nucleic acids.

6. (withdrawn) The array composition according to claim 5 wherein said nucleic acids comprise genomic DNA.

7. (withdrawn) The array composition according to claim 1 wherein said target analytes are proteins.

8. (withdrawn) The array composition according to claim 1 wherein said substrate is a fiber optic substrate.

9. (withdrawn) The array composition according to claim 1 wherein said substrate is plastic.

10. (withdrawn) The array composition according to claim 1 wherein said discrete sites are wells.

11. (withdrawn) The array composition according to claim 1, wherein said microspheres are randomly distributed on said surface.

12. (withdrawn) The array composition according to claim 1, wherein the microspheres of said first and second subpopulation each comprise a plurality of target analytes from a first and second target source, respectively.

13. (withdrawn) The array composition according to claim 13, wherein said first and second target source are first and second patients, respectively.

14. (currently amended) A method comprising:

a) providing an array composition comprising:

i) a substrate with a surface comprising discrete sites; and

ii) a population of microspheres comprising at least a first and a second subpopulation, wherein the microspheres of each subpopulation each comprise a plurality of different target analytes, and wherein a plurality of said different target analytes are covalently attached to each of said microspheres,

wherein said microspheres are distributed on said surface;

b) contacting said array composition with a first set of readout probes; and

c) detecting the presence of a first target analyte.

15. (original) The method according to claim 14 further comprising:

d) contacting said array composition with a second set of readout probes;

e) detecting the presence of a second target analyte.

16. (original) The method according to claim 14, wherein said microspheres are randomly distributed on said surface.

17. (original) The method according to claim 14, wherein said first set of readout probes comprises at least first and second readout probes, wherein said first and second readout probes comprise first and second labels, respectively.

18. (original) The method according to claim 17, further comprising detecting said first label as an indication of the presence of said first target analyte.

19. (previously presented) The method according to claim 14, 30, 31 or 32, wherein the microspheres of said first and second subpopulation each comprise a plurality of target analytes from a first and second target source, respectively.

20. (original) The array composition according to claim 19, wherein said first and second target source are first and second patients, respectively.

21. (currently amended) A method of genotyping comprising:

a) providing an array composition comprising:

i) a substrate with a surface comprising discrete sites; and

ii) a population of microspheres comprising at least a first and a second subpopulation, wherein the microspheres of each subpopulation each comprise at least first and second different target sequences covalently attached to each of said microspheres with first and second attachment moieties, respectively;

wherein said microspheres are randomly distributed on said surface;

b) contacting said array composition with a first set of extension probes that hybridize with at least said first target sequence adjacent to a first detection position to form an extension complex;

c) contacting said extension complex with a composition comprising

i) at least a first nucleotide;

ii) polymerase;

wherein said polymerase extends a first extension probe with said first nucleotide when said first nucleotide is complementary to said first detection position of said first target sequence; and

d) detecting the presence of said first nucleotide, whereby said genotype is determined.

22. (original) The method according to claim 21, wherein said first nucleotide comprises a label.

23. (currently amended) A method of determining the identification of a nucleotide at a detection position in at least a first target sequence comprising:

a) providing an array composition comprising:

i) a substrate with a surface comprising discrete sites; and

ii) a population of microspheres comprising at least a first and a second subpopulation, wherein the microspheres of each subpopulation each comprise a plurality of different target sequences, and wherein a plurality of said different target sequences are covalently attached to each of said microspheres, wherein said microspheres are distributed on said surface;

b) forming a first hybridization complex between said first target sequence and at least a first readout probe; and

c) determining the nucleotide at said detection position.

24. (previously presented) The method according to claim 23, wherein said target sequence comprises a first and a second target domain, wherein said first hybridization complex comprises said first target sequence, a first readout probe hybridized to said first domain and a second readout probe hybridized to said second domain, wherein at least one of said readout probes comprise a label said determining comprises adding a ligase to form a ligation complex.

25. (original) The method according to claim 24, wherein said first readout probe comprises a detectable label.

26. (original) The method according to claim 23, further comprising contacting said hybridization complex with at least a first nucleotide and a polymerase, wherein said

polymerase extends said first readout probe with said first nucleotide when said first nucleotide is complementary to said first detection position of said first target sequence.

27. (previously presented) The method according to claim 14, 21 or 23 wherein said substrate is a fiber optic bundle.

28. (previously presented) The method according to claim 14, 21 or 23 wherein said substrate is selected from the group consisting of glass and plastic.

29. (previously presented) The method according to claim 14, 21, or 23 further comprising contacting said microspheres with decoder binding ligands, wherein the microspheres of each subpopulation comprises an identifier binding ligand that will bind a decoder binding ligand for identification and elucidation of said target analyte.

30. (previously presented) The method according to claim 14, wherein said target analytes comprise target sequences.

31. (previously presented) The method according to claim 30, wherein said target sequences comprise target nucleic acids.

32. (previously presented) The method according to claim 31, wherein said target nucleic acids comprise target genomic DNA.

33. (previously presented) The method according to claim 21 and 23, wherein said target sequences comprise target nucleic acids.

34. (previously presented) The method according to claim 33, wherein said target nucleic acids comprise target genomic DNA.

35. (currently amended) A method comprising:

a) providing an array composition comprising:

i) a substrate with a surface comprising discrete sites; and

ii) a population of microspheres comprising at least a first and a second subpopulation, wherein the microspheres of each subpopulation each comprise a plurality

of different target analytes attached to each of said microspheres via receptor-ligand interaction, wherein said target analytes are derivatized with said receptor or said ligand, and wherein said microspheres are distributed on said surface;

b) contacting said array composition with a first set of readout probes; and

c) detecting the presence of a first target analyte.

36. (currently amended) A method of genotyping comprising:

a) providing an array composition comprising:

i) a substrate with a surface comprising discrete sites; and

ii) a population of microspheres comprising at least a first and a second subpopulation, wherein the microspheres of each subpopulation each comprise at least first and second different target sequences attached to each of said microspheres via receptor-ligand interaction; wherein said target analytes are derivatized with said receptor or said ligand,

wherein said microspheres are randomly distributed on said surface;

b) contacting said array composition with a first set of extension probes that hybridize with at least said first target sequence adjacent to a first detection position to form an extension complex;

c) contacting said extension complex with a composition comprising

i) at least a first nucleotide;

ii) polymerase;

wherein said polymerase extends a first extension probe with said first nucleotide when said first nucleotide is complementary to said first detection position of said first target sequence; and

d) detecting the presence of said first nucleotide, whereby said genotype is determined.

37. (currently amended) A method of determining the identification of a nucleotide at a detection position in at least a first target sequence comprising:

a) providing an array composition comprising:

i) a substrate with a surface comprising discrete sites; and

ii) a population of microspheres comprising at least a first and a second subpopulation, wherein the microspheres of each subpopulation each comprise a plurality of different target sequences attached to each of said microspheres via receptor-ligand interaction, wherein said target analytes are derivatized with said receptor or said ligand, wherein said microspheres are distributed on said surface;

b) forming a first hybridization complex between said first target sequence and at least a first readout probe; and

c) determining the nucleotide at said detection position.

38. (previously presented) The method according to claim 35, 36 or 37, wherein said receptor is streptavidin and said ligand is biotin.

39. (previously presented) The method according to claim 38, wherein said microspheres are streptavidin coated.